

GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test ($P(X \geq k)$), Benjamini-Hochberg FDR-corrected across all tested pairs. Corroborated Shared Genes: count of shared genes backed by ≥ 2 distinct disease_gdp.main_source values combined across both diseases (e.g. GWAS-backed for one, ClinVar-backed for the other still counts); Shared Gene Names lists each gene's own source count in parentheses. Overlap Coefficient: shared genes / MIN(each disease's own total gene count) -- complements the Jaccard-based Similarity Score by showing how much of the SMALLER disease's entire known gene-set is covered by this pair, which Jaccard (dividing by the union) can understate. Shared Cluster: cluster id if both diseases fall in the same label-propagation cluster (scripts/build_disease_clusters.php), blank otherwise. See scripts/build_related.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-11 03:00:14. Filters applied: disease name contains "Wolfram syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 07:47:45

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Deafness, aminoglycoside-induced	Wolfram syndrome	1	0	ND1 (1)	0.11111	0.33333	1.169e-3	1.895e-3	
Deafness, sensorineural, autosomal-mitochondrial type	Wolfram syndrome	1	0	ND1 (1)	0.12500	0.50000	7.792e-4	1.405e-3	
Other specified diabetes mellitus with unspecified complications	Wolfram syndrome	1	1	WFS1 (7)	0.14286	1.00000	3.897e-4	8.665e-4	
Wolfram syndrome	Wolfram-like syndrome	1	1	WFS1 (7)	0.14286	1.00000	3.897e-4	8.665e-4	
Turnpenny-fry syndrome	Wolfram syndrome	2	1	PCGF2 (5), CISD3 (1)	0.28571	1.00000	1.265e-7	8.712e-7	